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M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E	WT-ROS
M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E	SYNROS
M	T	D	M	A	T	G	N	A	P	E	L	L	V	E	ROS-R
M	T	E	T	A	Y	G	N	A	Q	D	L	L	V	E	ROS-AR
M	T	E	T	S	L	G	T	S	N	E	L	L	V	E	MUC-R
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	WT-ROS
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	SYNROS
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	ROS-R
L	T	A	D	I	V	A	A	Y	V	S	N	H	V	V	ROS-AR
L	T	A	E	I	V	A	A	Y	V	S	N	H	V	V	MUC-R
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A	WT-ROS
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A	SYNROS
P	V	S	D	L	A	N	L	I	S	D	V	H	S	A	ROS-R
P	V	T	E	L	P	G	L	I	S	D	V	H	T	A	ROS-AR
P	V	A	E	L	P	T	L	I	A	D	V	H	S	A	MUC-R
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E	WT-ROS
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E	SYNROS
L	S	N	T	S	V	P	Q	P	A	A	A	V	V	E	ROS-R
L	S	G	T	S	A	P	A	S	V	A	V	N	V	E	ROS-AR
L	N	N	T	T	A	P	A	P	V	V	V	P	V	E	MUC-R
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D	WT-ROS
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D	SYNROS
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	E	ROS-R
K	Q	K	P	A	V	S	V	R	K	S	V	Q	D	D	ROS-AR
K	P	K	P	A	V	S	V	R	K	S	V	Q	D	D	MUC-R
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K	WT-ROS
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K	SYNROS
Q	I	T	C	L	E	C	G	G	N	F	K	S	L	K	ROS-R
H	I	V	C	L	E	C	G	G	S	F	K	S	L	K	ROS-AR
Q	I	T	C	L	E	C	G	G	T	F	K	S	L	K	MUC-R
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R	WT-ROS
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R	SYNROS
R	H	L	M	T	H	H	S	L	S	P	E	E	Y	R	ROS-R
R	H	L	T	T	H	H	S	M	T	P	E	E	Y	R	ROS-AR
R	H	L	M	T	H	H	N	L	S	P	E	E	Y	R	MUC-R
E	K	W	D	L	P	V	D	Y	P	M	V	A	P	A	WT-ROS
E	K	W	D	L	P	V	D	Y	P	M	V	A	P	A	SYNROS
E	K	W	D	L	P	T	D	Y	P	M	V	A	P	A	ROS-R
E	K	W	D	L	Q	V	D	Y	P	M	V	A	P	A	ROS-AR
D	K	W	D	L	P	A	D	Y	P	M	V	A	P	A	MUC-R
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	WT-ROS
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	SYNROS
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	ROS-R
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	ROS-AR
Y	A	E	A	R	S	R	L	A	K	E	M	G	L	G	MUC-AR
Q	R	R	K	A	N	R									WT-ROS
Q	R	R	K	A	N	R	P	K	K	K	R	K	V		SYNROS
Q	R	R	K	R	G	R	G								ROS-R
Q	R	R	K	A	N	R									ROS-AR
Q	R	R	K	R	R	G	K								MUC-AR

FIG. 1A

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GCGGATCCCC	GGGTATGACT	GAGACTGCTT	ACGGTAACGC
TCAGGATCTT	CTTGTTGAGC	TTACTGCTGA	TATCGTTGCT
GCTTACGTTT	CTAACCACGT	TGTTCCCTGTT	ACTGAGCTTC
CTGGACTTAT	CTCTGATGTT	CATACTGCAC	TTTCTGGAAC
ATCTGCTCCT	GCTTCTGTTG	CTGTTAACGT	TGAGAAGCAG
AAGCCTGCTG	TTTCTGTTCG	TAAGTCTGTT	CAGGATGATC
ATATCGTTTG	TTTGGAGTGT	GGTGGTTCTT	TCAAGTCTCT
CAAGCGTCAC	CTTACTACTC	ATCACTCTAT	GACTCCAGAG
GAGTATAGAG	AGAAGTGGA	TCTTCCTGTT	GATTACCCTA
TGGTTGCTCC	TGCTTACGCT	GAGGCTCGTT	CTCGTCTCGC
TAAGGAGATG	GGTCTCGGTC	AGCGTCGTAA	GGCTAACCGT
CCAAAAAAGA	AGCGTAAGGT	CTGAGAGCTC	GC

FIG. 1B

M T E T A Y G N A Q D L L V E
ATG ACN GAR ACN GCN TAY GGN AAY GCN CAR GAY YTN YTN GTN GAR

L T A D I V A A Y V S N H V V
YTN ACN GCN GAY ATH GTN GCN GCN TAY GTN WSN AAY CAY GTN GTN

P V T E L P G L I S D V H T A
CCN GTN ACN GAR YTN CCN GGN YTN ATH WSN GAY GTN CAY ACN GCN

L S G T S A P A S V A V N V E
YTN WSN GGN ACN WSN GCN CCN GCN WSN GTN GCN GTN AAY GTN GAR

K Q K P A V S V R K S V Q D D
AAR CAR AAR CCN GCN GTN WSN GTN MGN AAR WSN GTN CAR GAY GAY

H I V C L E C G G S F K S L K
CAY ATH GTN TGY YTN GAR TGY GGN GGN WSN TTY AAR WSN YTN AAR

R H L T T H H S M T P E E Y R
MGN CAY YTN ACN ACN CAY CAY WSN ATG ACN CCN GAR GAR TAY MGN

E K W D L P V D Y P M V A P A
GAR AAR TGG GAY YTN CCN GTN GAY TAY CCN ATG GTN GCN CCN GCN

Y A E A R S R L A K E M G L G
TAY GCN GAR GCN MGN WSN MGN YTN GCN AAR GAR ATG GGN YTN GGN

Q R R K A N R P K K K R K V
CAR MGN MGN AAR GCN AAY MGN CCN AAR AAR AAR MGN AAR GTN

FIG. 1C

ROS Inverted Repeat
DNA Binding Sites(Operator sequences)

TATATTTCAA-TTTTA-TTGTAATATA	<i>virC/virD</i>
***** ** ** * *** *** **	
TATAATTAAAATATTAAGTCGCATT	<i>ipt</i>

FIG. 1D

Comparison of ROS DNA Binding Site (Operator) Sequences

<i>VirC/VirD</i>	TATATTTCAA
	TATATTACAA
<i>ipt</i>	TATAATTAAA
	AATGCGACAG
	TATAHTtCAA
	a g gaa g
Consensus	WATDHWKMAR

FIG. 1E

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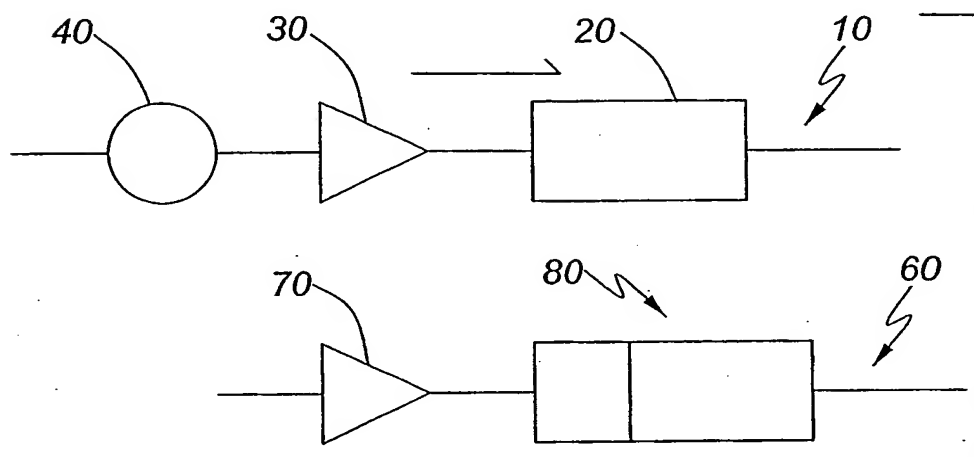


FIG. 2A

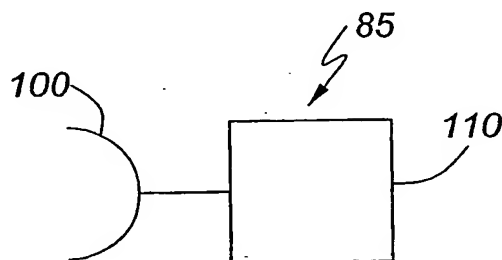


FIG. 2B

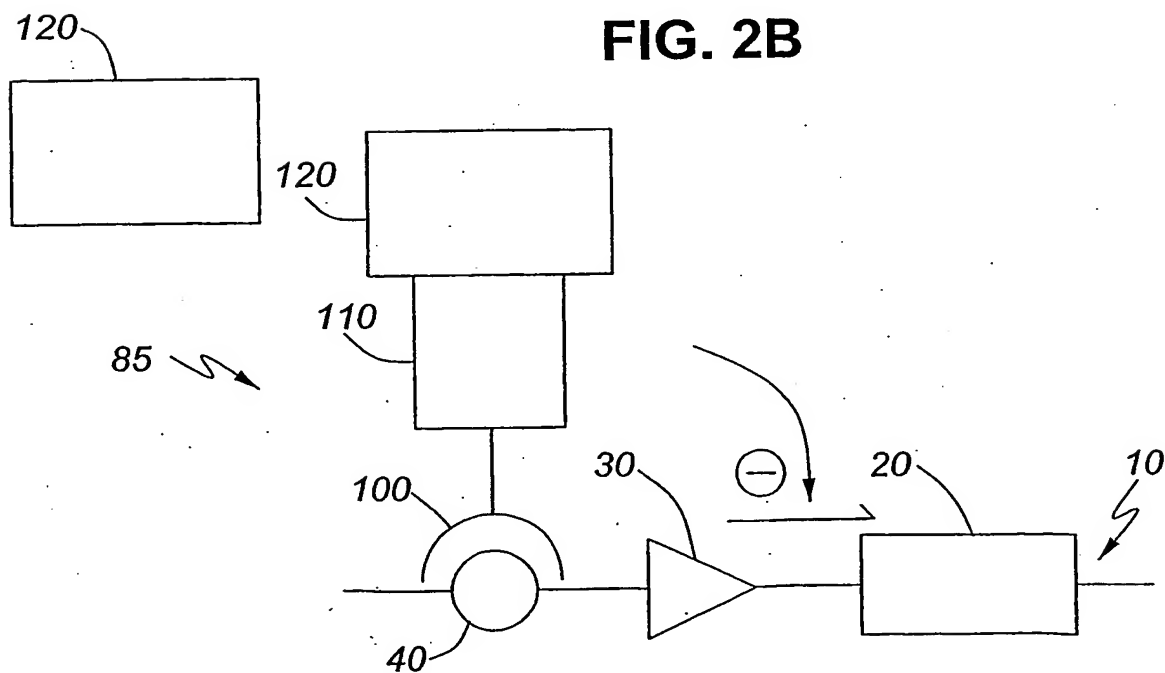


FIG. 2C

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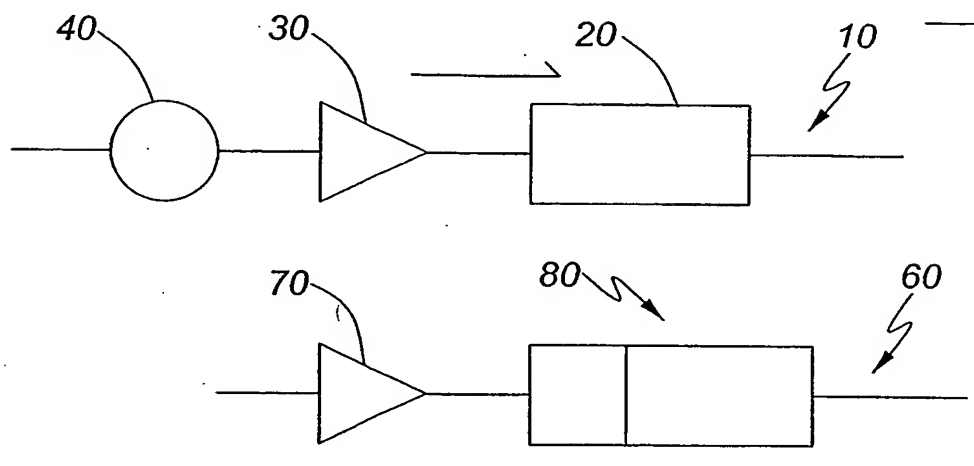


FIG. 3A

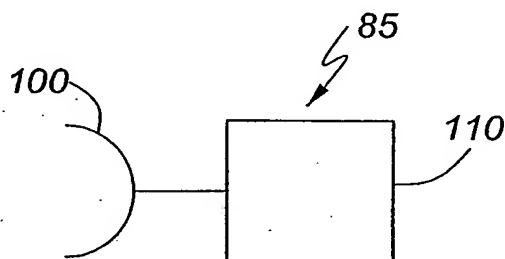


FIG. 3B

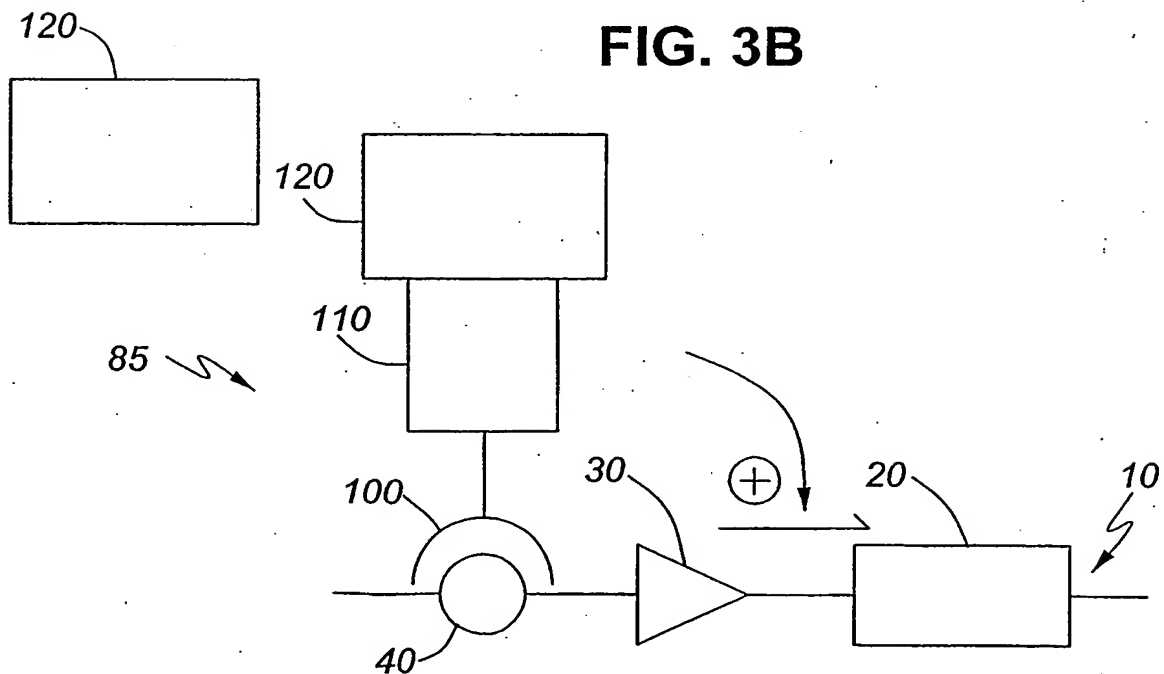


FIG. 3C

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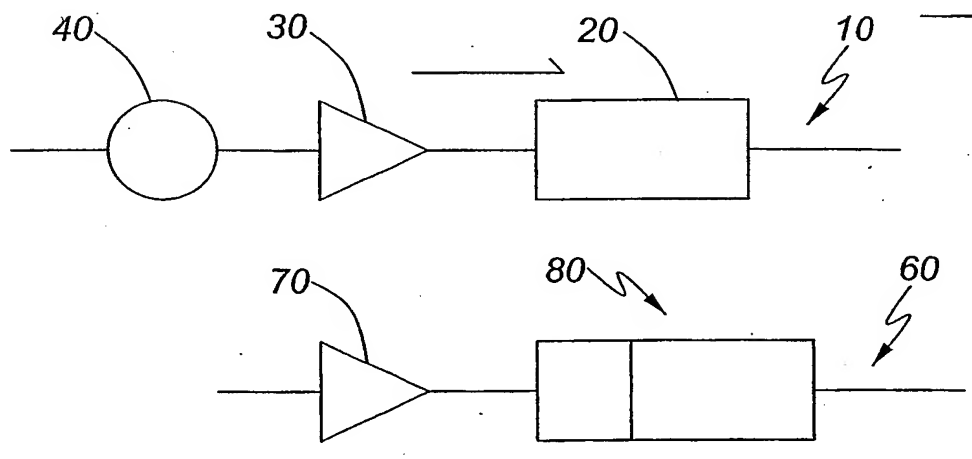


FIG. 4A

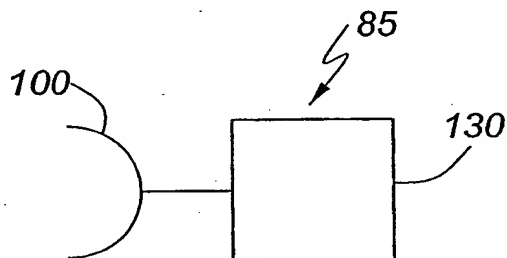


FIG. 4B

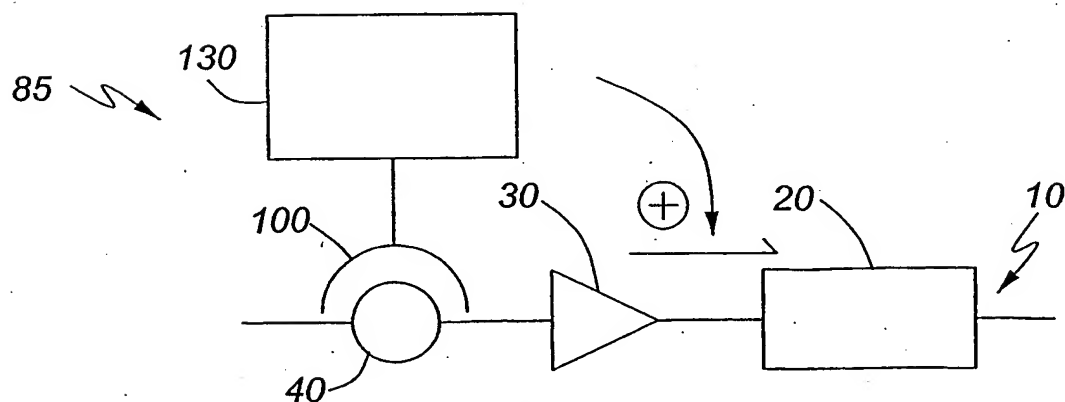
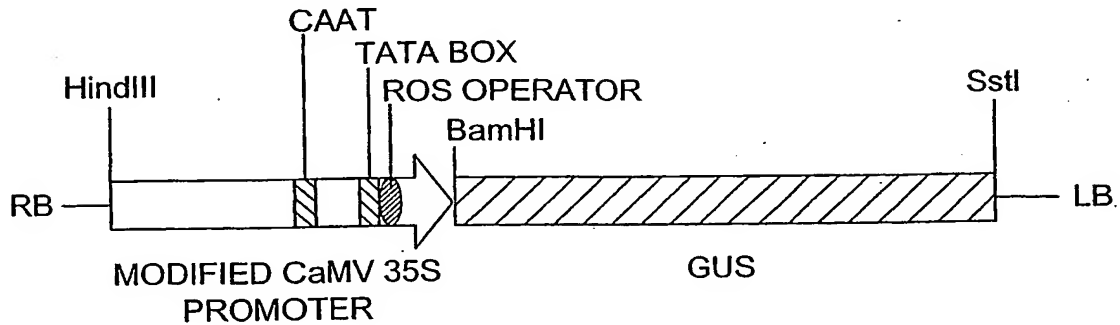


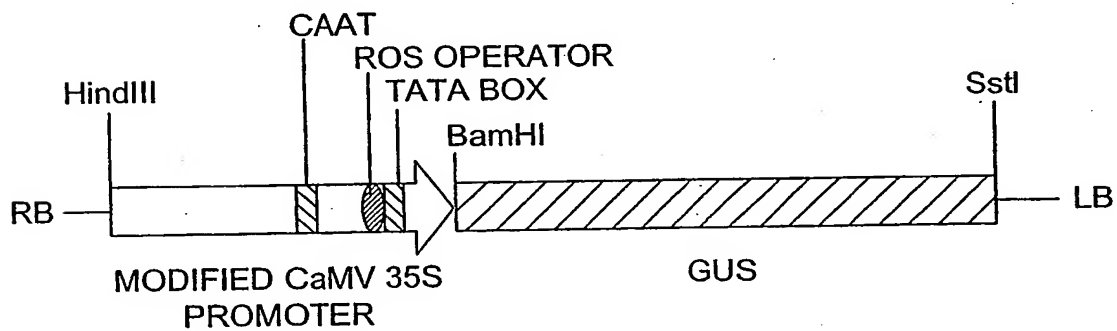
FIG. 4C

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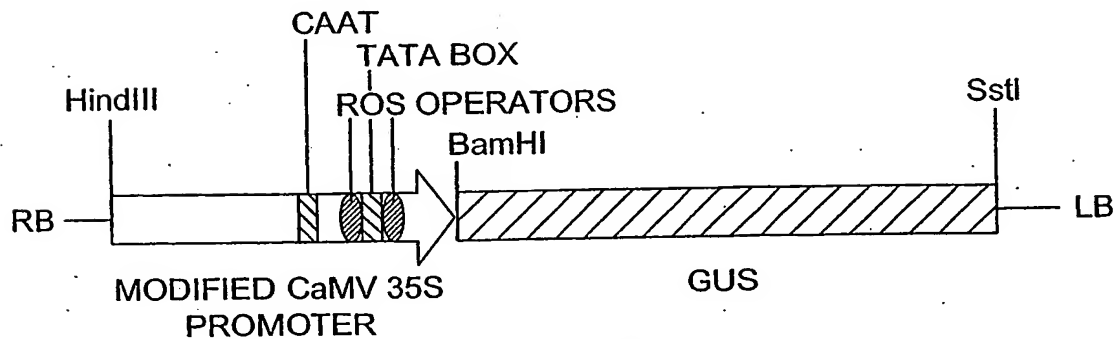
p74-315

FIG. 5A



p74-316

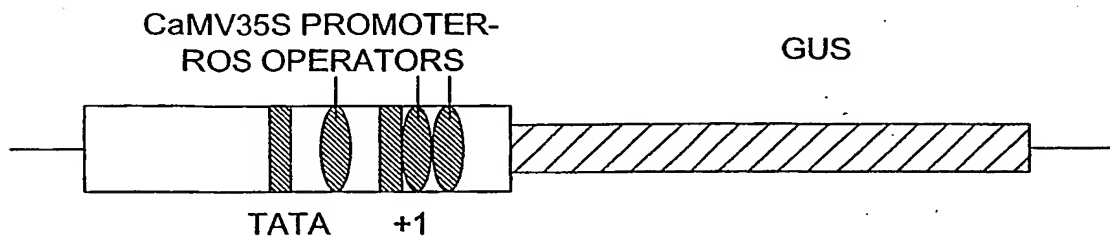
FIG. 5B



p74-309

FIG. 5C

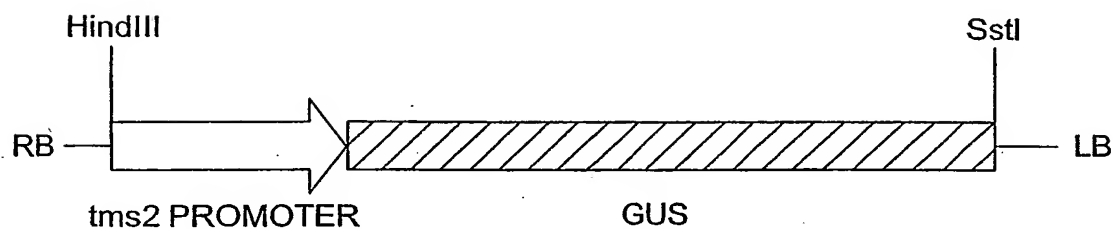
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p74-118

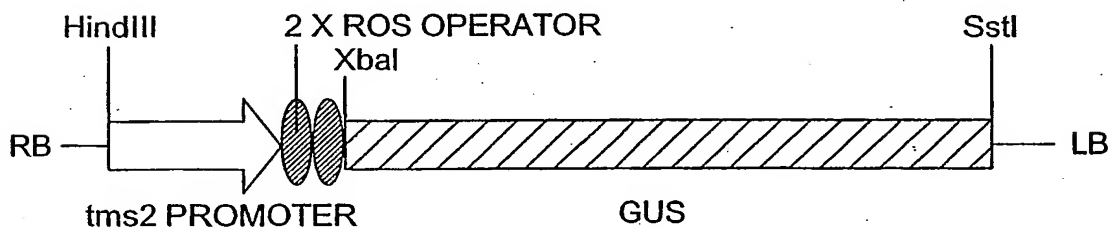
FIG. 5D

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p76-507

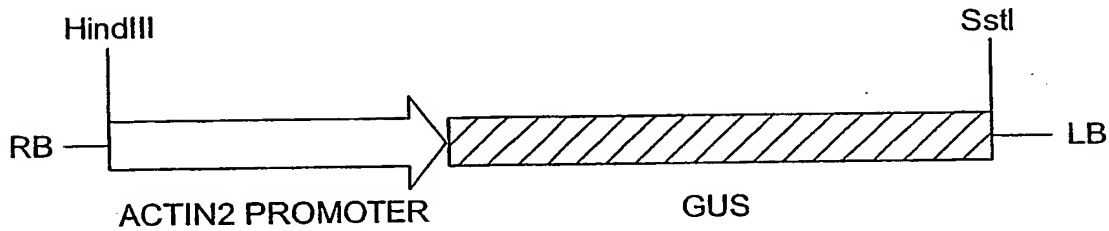
FIG. 6A



p76-508

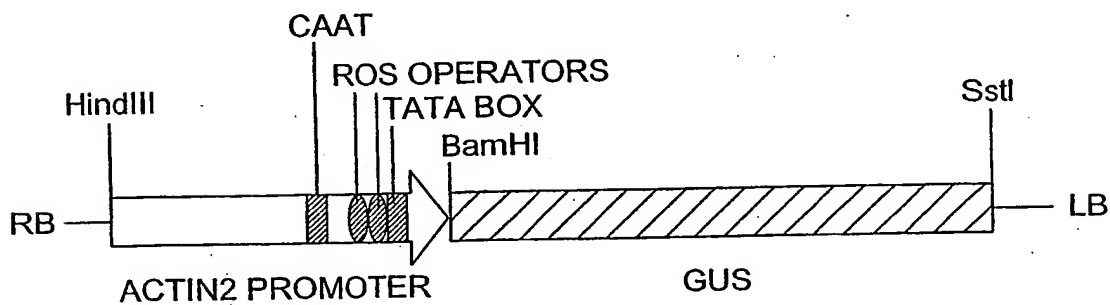
FIG. 6B

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p75-101

FIG. 7A



p74-501

FIG. 7B

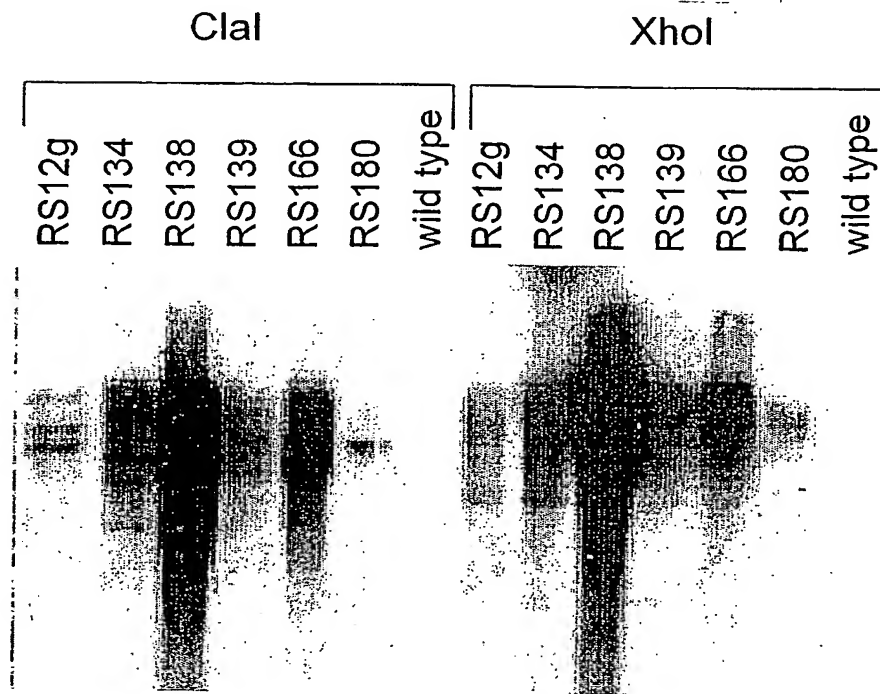


FIG. 8A

P74-101

RS 91

RS 93

RS 121

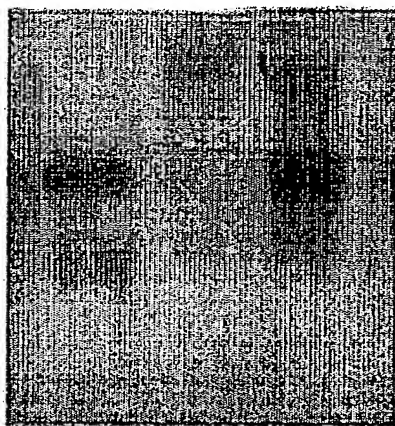


FIG. 8B

Columbia wt

pB1121



p74-501



buffer

FIG. 9

bnKCP (1) M-AGGGPTFSIELSAYG-SDLPDKASGDIP-----NEEGSGLSRVSGSIW
atKCP (1) MELMAKPTFSIEVSQYGTDLPLATEKASSSSSSFETTNEEG-VEESGLSRIW
atKCL1 (1) M-----EVLVGSTFRDRSSVTTHDQAVP-----AS-LSSRIGLRRC
atKCL2 (1) M--VGSSFGIGMAAYVRDHGRVSAQDKAVQTALFLADESGRGGSQIGIGLR

bnKCP (45) SG----RTVDYSSSESSSIGTPGDSEEEDEESEEDNDEEEL-----GLASL
atKCP (52) SG----QTADYSSDSSS-IGTPGDSEEEDEESENENDDVSSKELGLRGLASM
atKCL1 (36) GR-----SPPPESSSVGETSENEEEDDAVSSSQGRWLN-----SFS
atKCL2 (50) MSNNNNKSPEESSDSSSIGESSENEEEEEEDDAVSCQRTLD-----SFS

bnKCP (87) RSLEDSLPSK-GLSSHYKGKSKSFGNLGEIG-SVKEVPKQENPLNKKRRRLQI
atKCP (99) SSLEDSLPSKRGLSNHYKGKSKSFGNLGEIG-SVKEVAKQENPLNKKRRRLQI
atKCL1 (74) SSLEDSLPIKRGLSNHYIGKSKSFGNLMEAS-NTNDLVKVESPLNKKRRRLLI
atKCL2 (96) SSLEDSLPIKRGLSNHYVGKSKSFGNLMEAAASKAKDLEKVENPFNKKRRRLVI

bnKCP (137) YNKLARKS-----FYSWQNPKSMPLLPVHEDNDDEEGDDG-----
atKCP (150) CNKLARKS-----FYSWQNPKSMPLLPVNEDEDDDDDEEDLKSGFDEN
atKCL1 (125) ANKLRRRSSLSFSFIYTKINPNSMPLIALQESDNEDHKLNDDDDDDDS---S
atKCL2 (148) ANKLRRR-----GRSITYEEDHHIHNDYEDDDG-----

bnKCP (172) -DLSDEERGVDVLARRPSFKNRALKSMSCFALSDLQEEEE---EEEDE
atKCP (196) KSSSDEEGVKVVRKGSFKNRAYKSRSCFALSDLIEED---DDDDQ
atKCL1 (174) SDETSKLKEKRMKMTNHRDFMVPQTKSCFSLTSFQDDDDR-----
atKCL2 (177) ----DGDDHRKIMMMKNKKELMAQTRSCFCLSSLQEEDDGDDDEDE

FIG. 10A

Fig. 10B

bnKCP GDDGDLSDDEERG GGDVLR RPSFKNRALKSMSCFALSDLQEEE
ATF-1 DSSDSIGSSQQA HGILARRPSYRKILKDLSSDTRGRKGDGE
hyCREB ESVD SVTDSQKRREILSR RPSYRKILNDLSSDAPGVPRIEEE
CREB ESVD SVTDSQKRREILSR RPSYRKILNDLSSDAPGVPRIEEE
CREM SADSEVIDSHKRREILSR RPSYRKILNELSSDVP GIPKIEEEE
cCREM AESEGVIDSHKRREILSR RPSYRKILNELSSDVP GVPKIEEEE

Fig. 10C

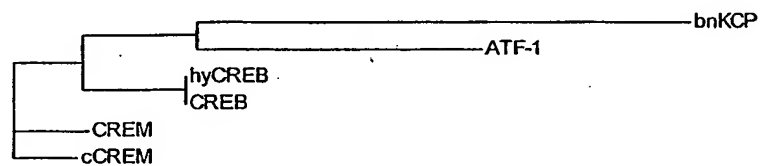


FIG. 10

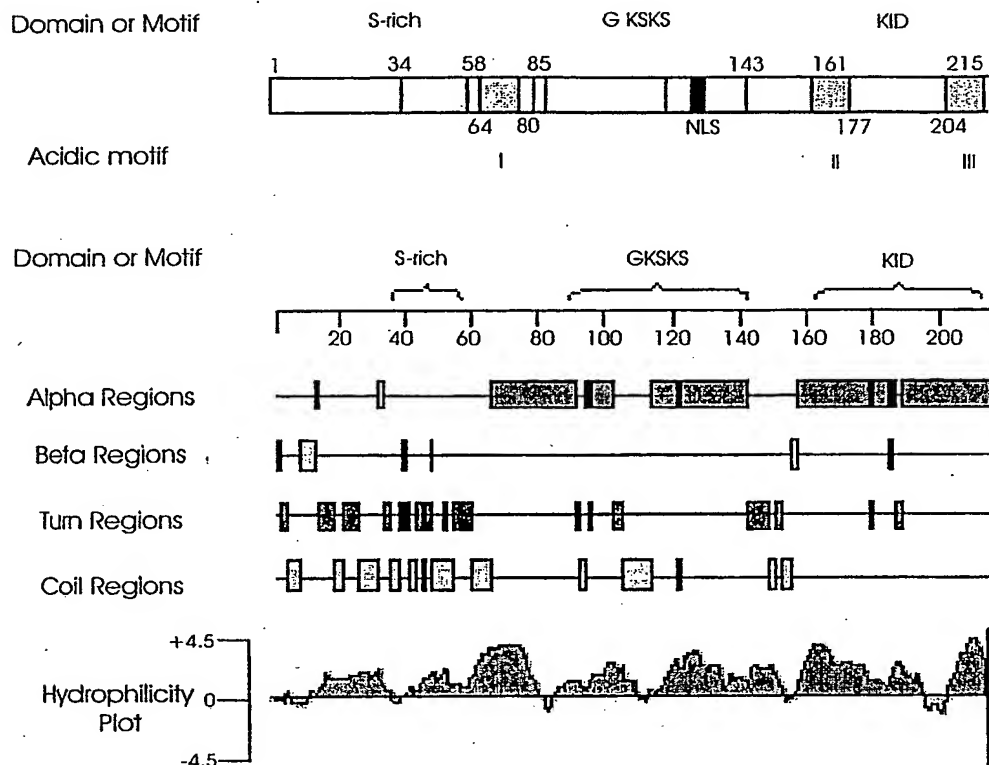


FIG. 11

EI X H P EV K

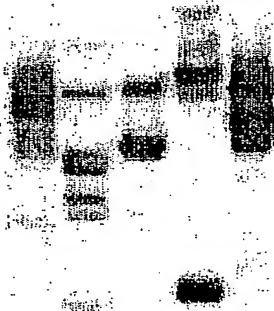


FIG. 12

Fig. 13A

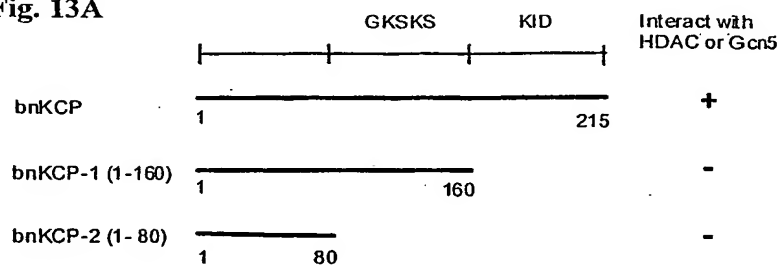


Fig. 13B

	10% input	GST-HDAC	GST-Gcn5	GST
bnKCP	+	+	+	+
bnKCP-1 (1-160)	+	+	+	+
bnKCP-2 (1-80)	+	+	+	+
no template	+			
luciferase	+			



FIG. 13

Fig. 13C-1

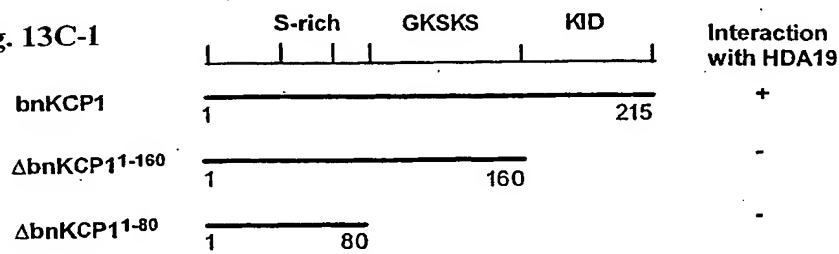


Fig. 13C-2

	10% input	GST-HDA19	GST
bnKCP1	+	+	+
Δ bnKCP1 ¹¹⁻¹⁶⁰	+	+	+
Δ bnKCP1 ¹¹⁻⁸⁰	+	+	+
no template			
luciferase			



Fig. 13C-3

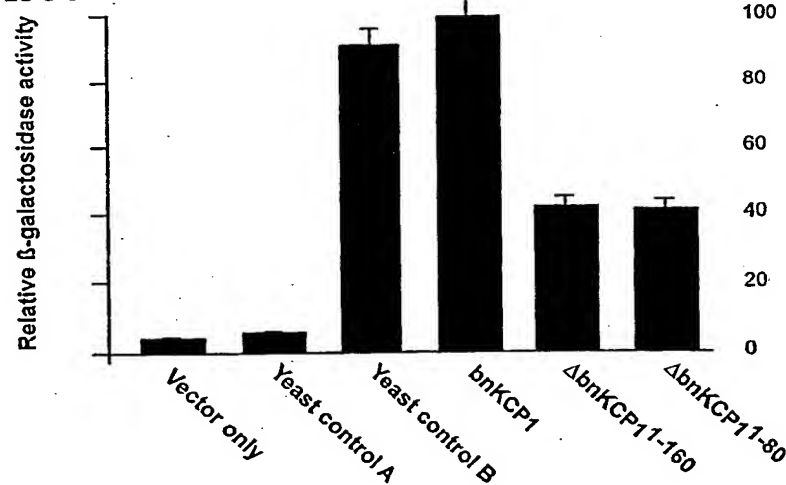


FIG. 13 cont'd

Fig. 14A

Wild type KID GDDGDLSD~~E~~ERG~~G~~GDVLARR~~P~~SFKNRALKSMSCFALSDLQEEE
(RRPS¹⁸⁸)
↓
Mutant KID GDDGDLSD~~E~~ERG~~G~~GDVLARR~~P~~GFKNRALKSMSCFALSDLQEEE
(RRPG¹⁸⁸)

Fig. 14B

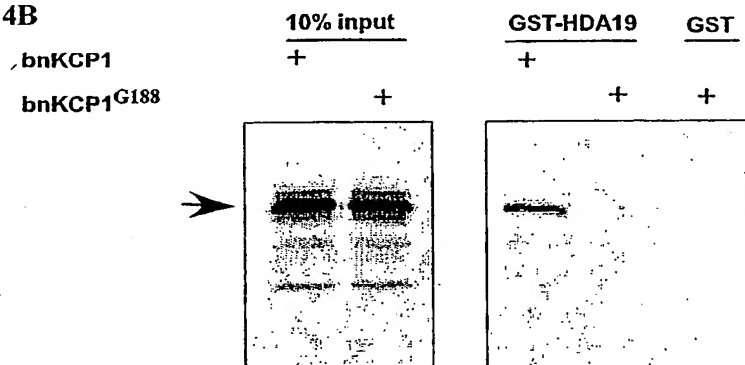


FIG. 14

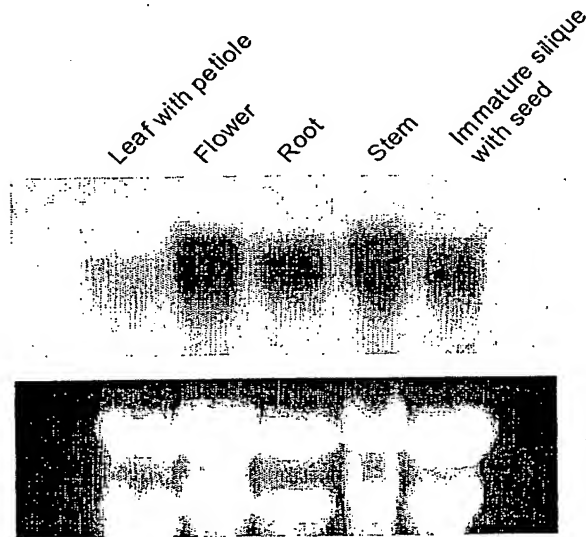
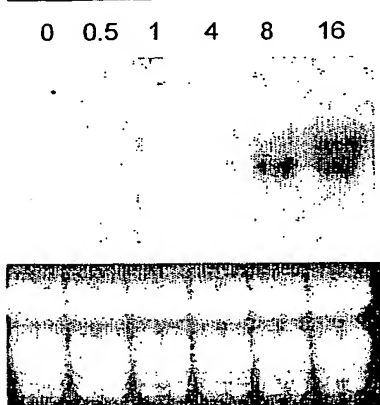


FIG. 15

Fig. 16A

Cold Treatment (h) – Leaf Blade



Cold Treatment (h) – Stem

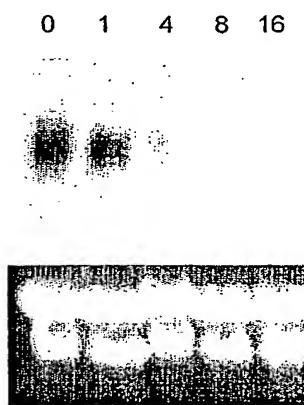


Fig. 16B

LaCl₃ Treatment (h)

Inomycin Treatment (h)

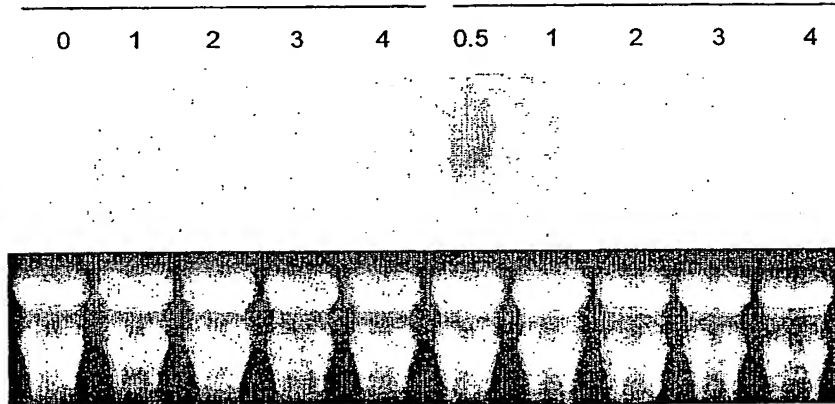


FIG. 16

Fig. 17A

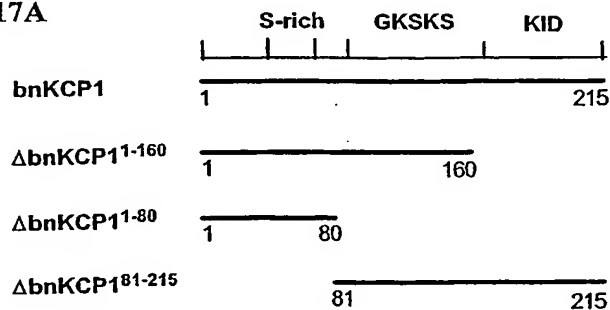


Fig. 17B

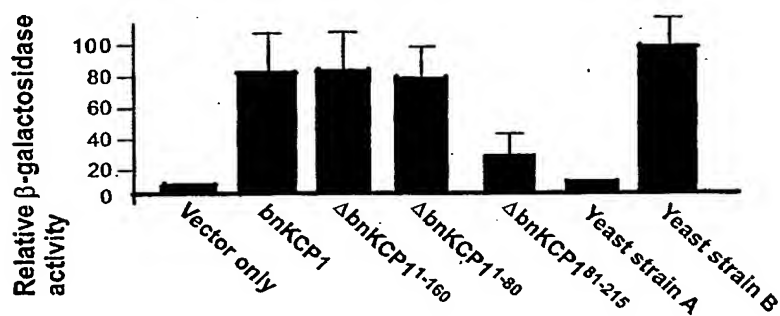


FIG. 17

Fig. 18A

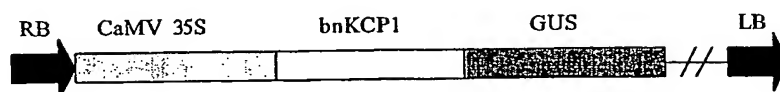


Fig. 18B

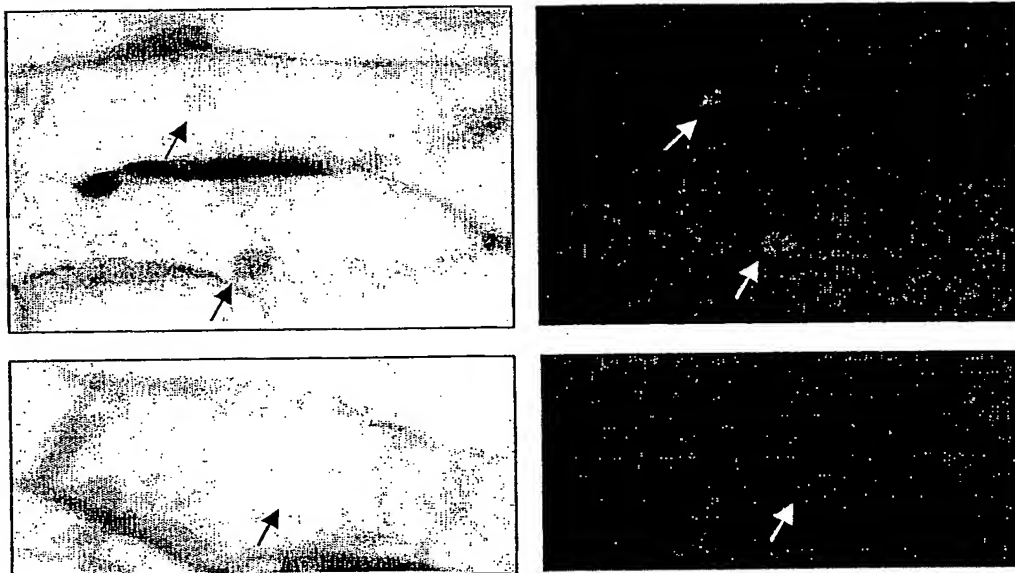


FIG. 18

Strategy for cloning zinc finger domain fusion with KID

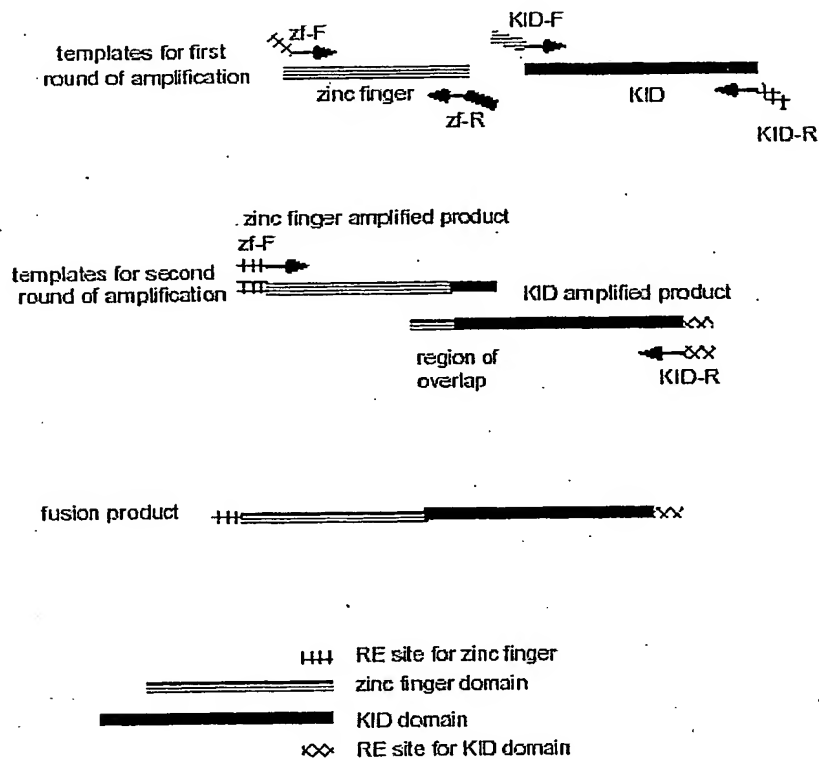


FIG. 19

BnSCL1	(1)	MKLOASSPODNO-----PSNT-----
AtSCL15	(1)	MKIPASSPODIT-----NNNN-----
LeSCL	(1)	MKVRFSTNDNVSSKPLVNSNNSFTFPAATNGSNLCYEPKSVLELRRSPSP
BnSCL1	(17)	-----TNNSTDSNHLSMDEHVMR-SMDWDSIMKELEVDDDSA
AtSCL15	(17)	-----NTNSTDSNHLSMDEHVMR-SMDWDSIMKELELDDDSA
LeSCL	(51)	IVDKQIITTNPDLSALCGGEPLOLCDEVLNSNFEWDWSLMRELGLDDSA
BnSCL1	(53)	PYQLQP---S---S-----FNLPEED-----IDSSDVYEGPN
AtSCL15	(53)	ENSLKTGFTTTTTDSTILPIYAVDSNLEGFEDQIQPSDFESSSDVYEGON
LeSCL	(101)	SLSKTNPLTHSESLTQFHNISEFSAESNOEFSPDFSFSDTNFPOQFPTVN
BnSCL1	(80)	QITGYGENSLDSVDNG----GFDYLEDLIRVVDCTESDELHLAHVVLSQL
AtSCL15	(103)	QITGYGENSLDSVDNG----GFDYLEDLIRVVDCTESDELQLAGVVLSQL
LeSCL	(151)	QASFINALELSGDIHQNWSVGFDYVDELIRFACCEETNAQOLAHVILARI
		LHRI
BnSCL1	(126)	NORLOTSAGRPLORAAFYFKEALGSLTCTNRN---QTFSSWDIVOKIRAT
AtSCL15	(149)	NORLRSEAGRPLORAAFYFKEALGSLTCTNRNPIRLSSWSEIVORIRAT
LeSCL	(201)	NORLRSAAGKPLORAAFYFKEALQALGASARQT-RSSSSSDVIOIKSY
BnSCL1	(174)	KEFSGISPIPLFSHFTANOAILDSLSSQSSSPFVHVVDTEIGFGGQYASL
AtSCL15	(199)	KEYSGISPIPLFSHFTANOAILDSLSSQSSSPFVHVVDTEIGFGGQYASL
LeSCL	(250)	KILSNISPIPLFSSFTANOAVLEAVDG---SMFVHVIDEIGIGGHWASE
		VHIIID
BnSCL1	(224)	MRELAEEKS-----ANGGFLRVTAVVAEDCAVETRLVKENLTQFAAEMKIRE
AtSCL15	(249)	MRELAEEKS-----VSGGFLRVTAVVAECCAVETRLVKENLTQFAAEMKIRE
LeSCL	(297)	MKELADKAECKRANAPILRITALVPEEYAVESRLIRENLTQFAELNIGF
		LHRII
BnSCL1	(270)	QTEFVLMKTFEILSEKATREVDGERTIVVLISPAIFRRVIGTAEFVNNLGR
AtSCL15	(295)	QTEFVLMKTFEMLSEKATREVEGERTIVVLISPAIFRRLSGITDFVNNLRR
LeSCL	(347)	EIDFVLIRTFELLSFKATKEMECEKTIVVLISPAIFRRVG---SEFVNNLRR
BnSCL1	(320)	VSPNVVVVVDSEGCPEITAGSGSFRREEVSAHEFYTMVLESIDAAAPPFC--
AtSCL15	(345)	VSPNVVVVVDSEGCWTEITAGSGSFRREEVSAHEFYTMVLESIDAAAPPFC--
LeSCL	(395)	ISPNVVVVVDSEGLMGYG-AMSERQTVIDGLEFYSTLLESTFANIGCGN
		PFYRE
BnSCL1	(368)	-DLVKKTIVETFLRPKISAAVETAANRRSAGOMTWREMLCAAGMRPVOLS
AtSCL15	(393)	-DLVKKTIVAEFVLRPKISAAVETAADRRTIGEMTWREAFCAAGMRPIQOS
LeSCL	(444)	CEDWMRKIENFVLPKIVDMIGAVG--RRGGGGSWRDAMVDAGERPVGTS
		SAW
BnSCL1	(417)	QFADFQAECLLEKAQVRGFHVAKRQGEVLVLCWHGRALVATSANRE
AtSCL15	(442)	QFADFQAECLLEKAQVRGFHVAKRQGEVLVLCWHGRALVATSANRE
LeSCL	(492)	QFADFQADCLLGRVQVRGFHVAKROAEMLLCWHGRALVATSANRC

FIG. 20

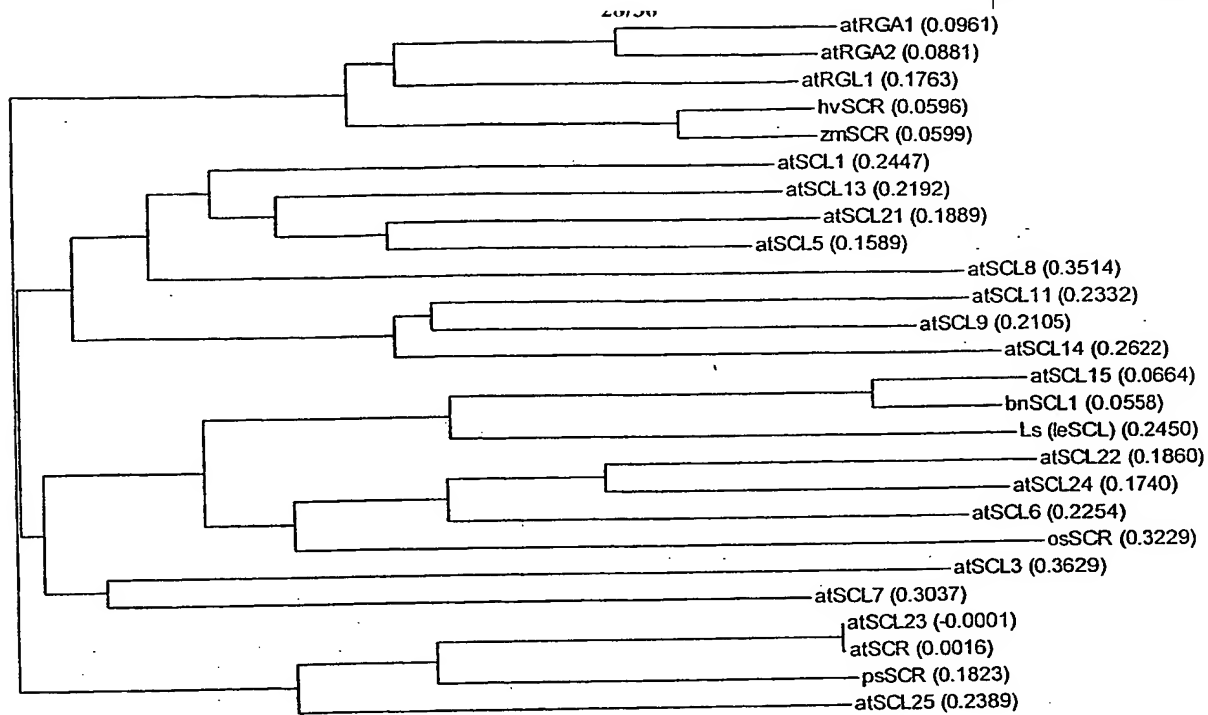


FIG. 21

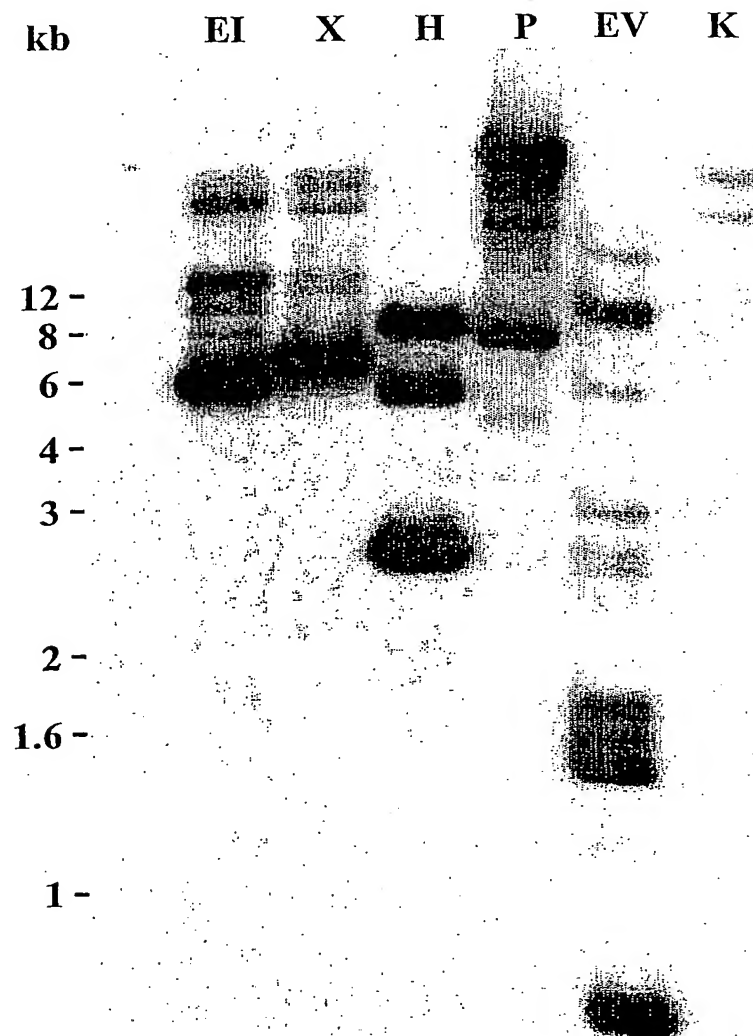


FIG. 22

Fig. 23A

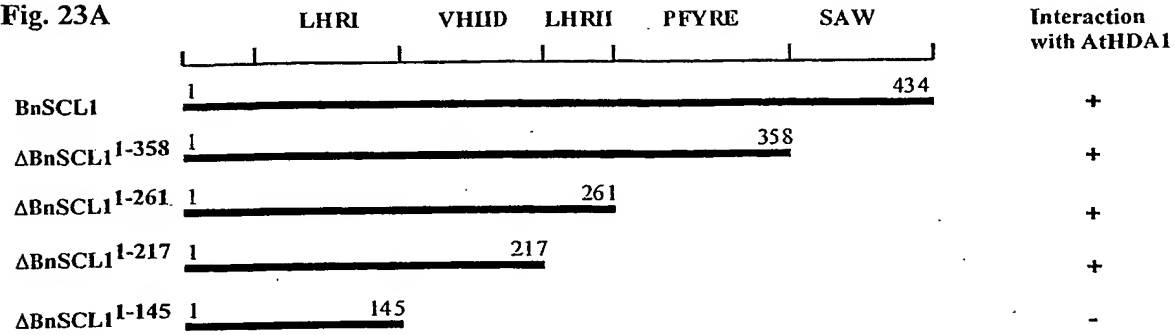


Fig. 23B

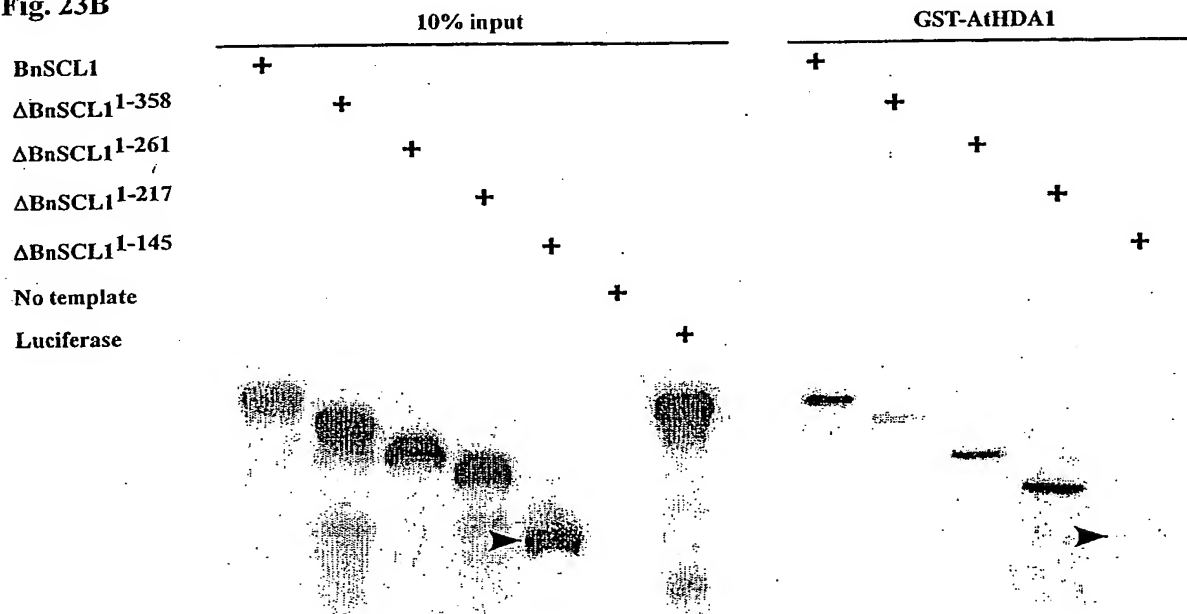


FIG. 23

Fig. 24A

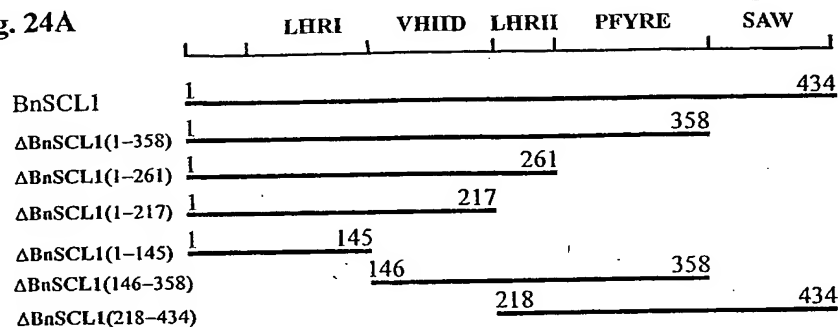


Fig. 24B

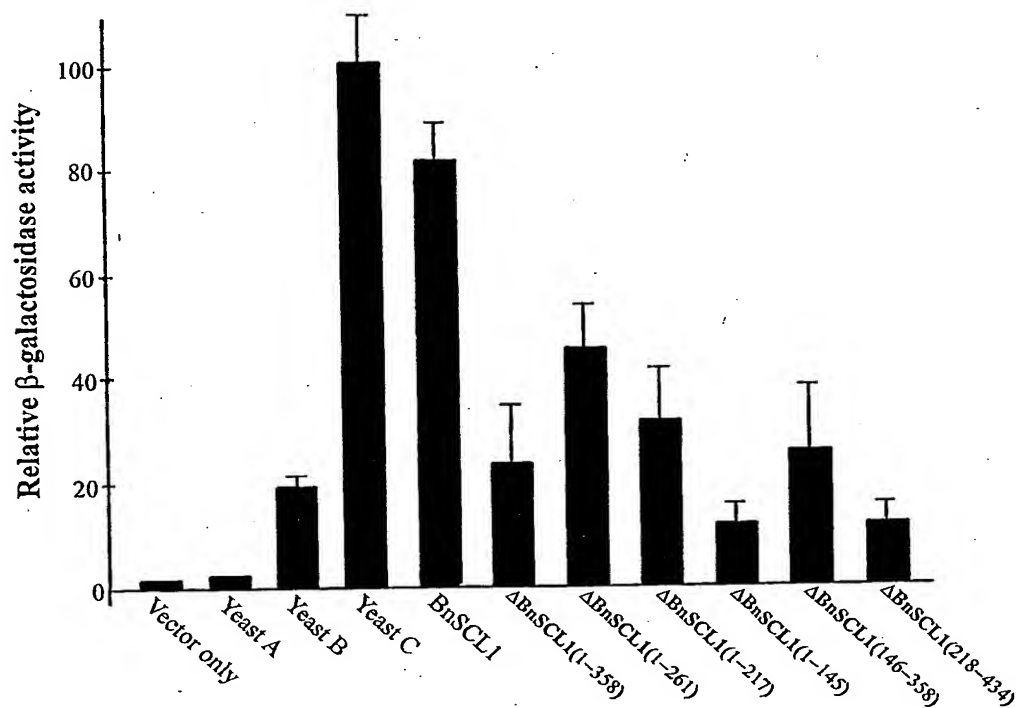


FIG. 24

Fig. 25A

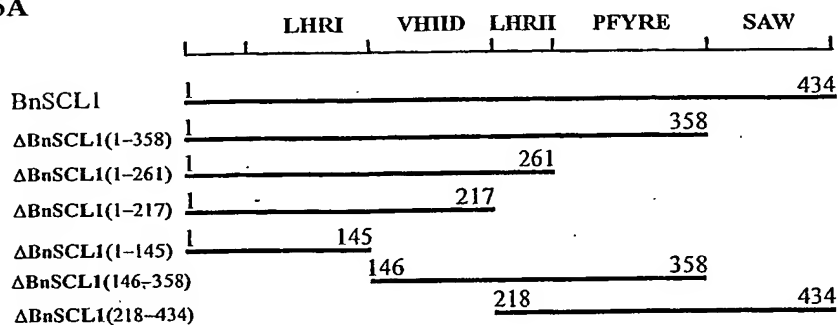


Fig. 25B

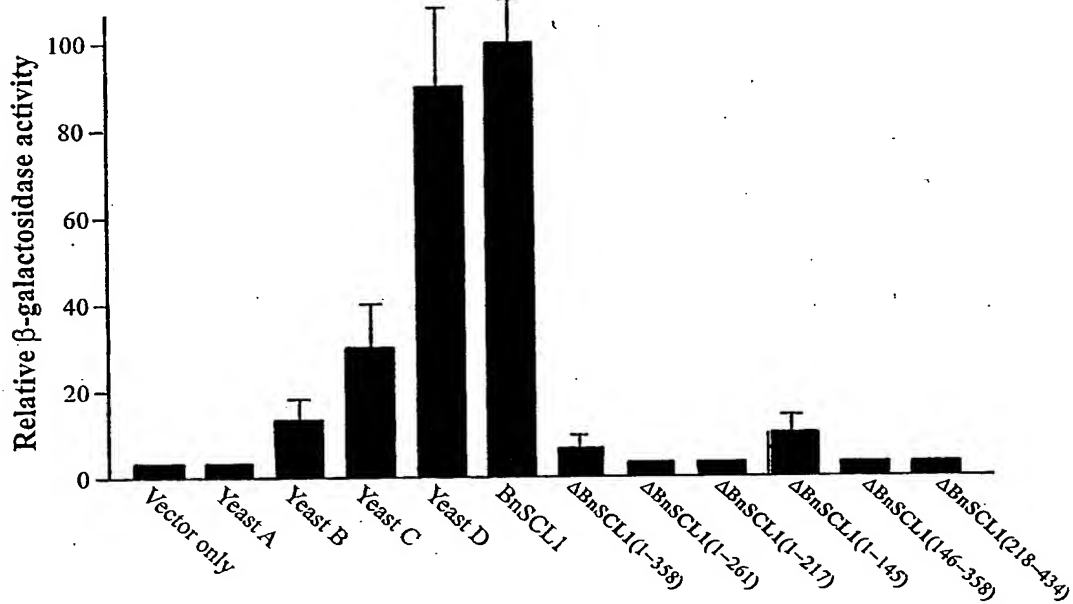


FIG. 25

Fig. 26A

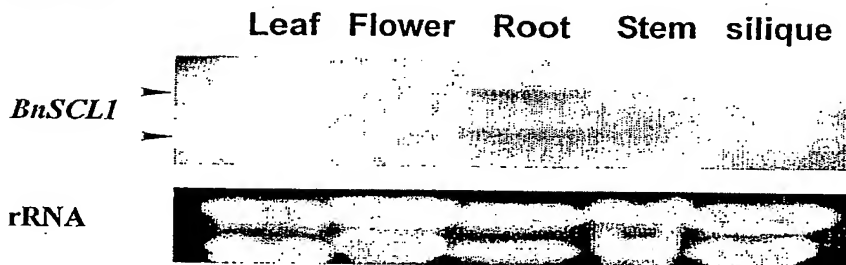


Fig. 26B

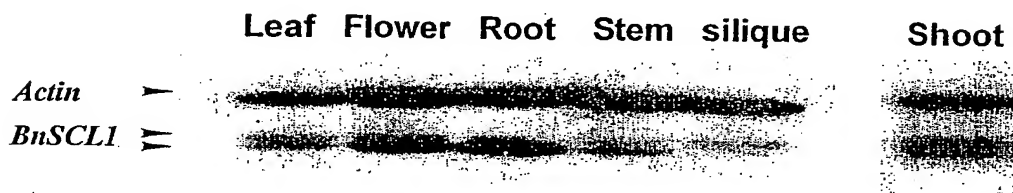


FIG. 26

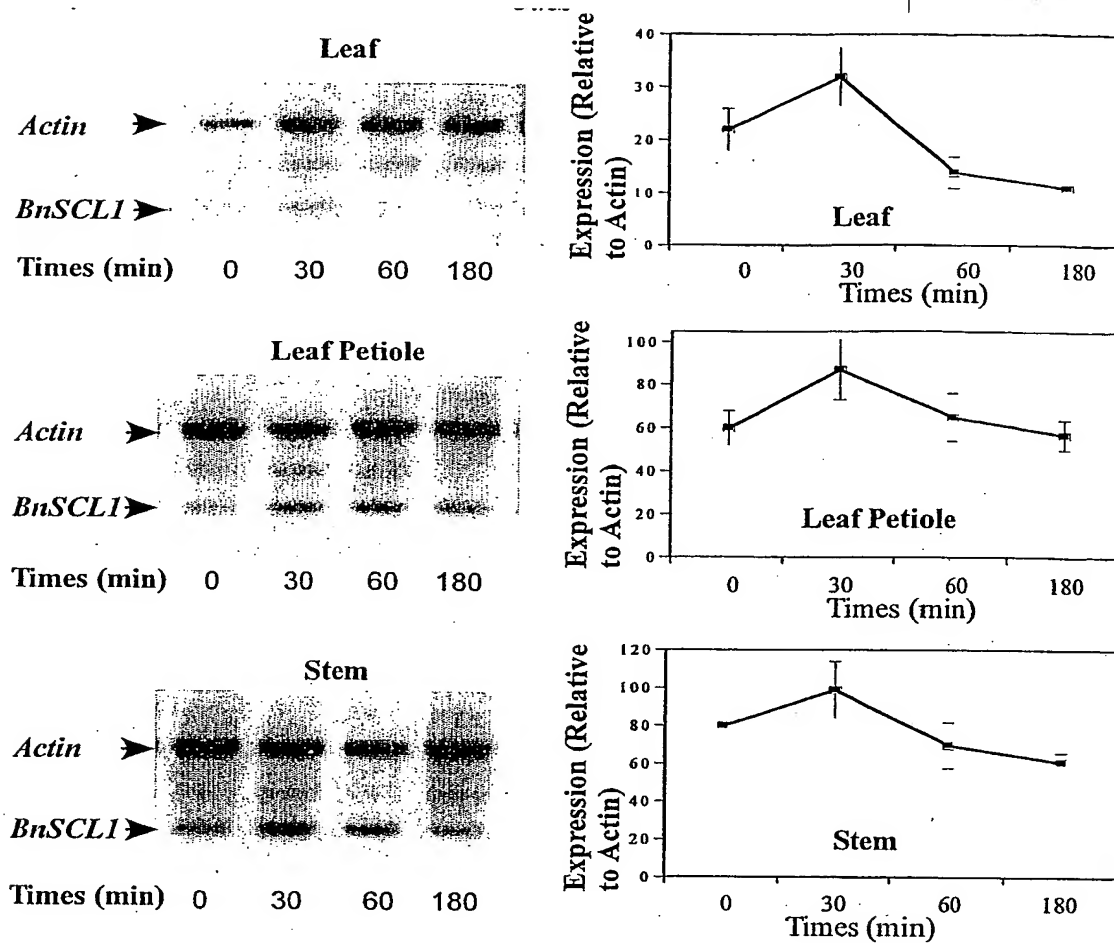


FIG. 27

Fig. 28A

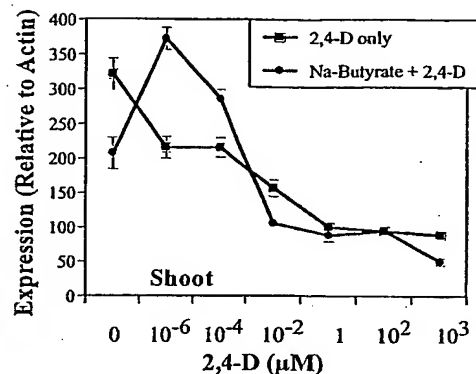
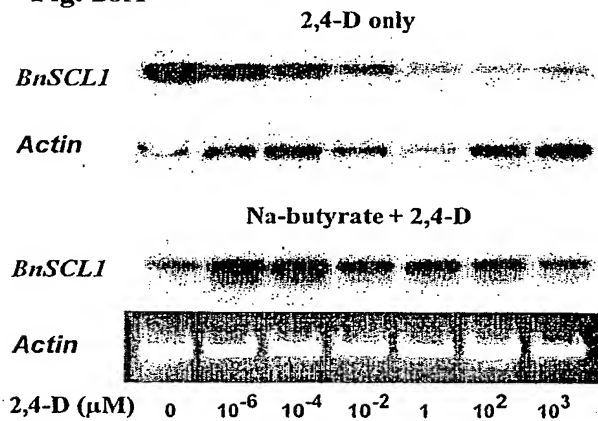


Fig. 28B

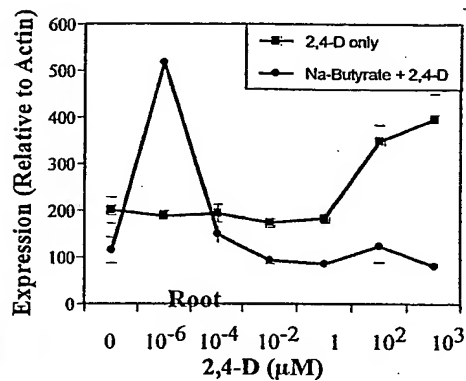
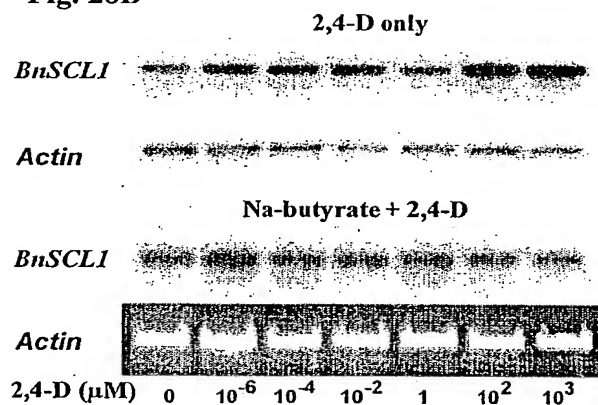


Fig. 28C

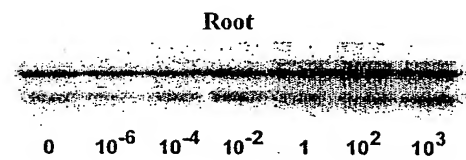
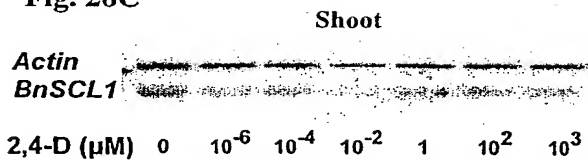


FIG. 28

Fig. 29A

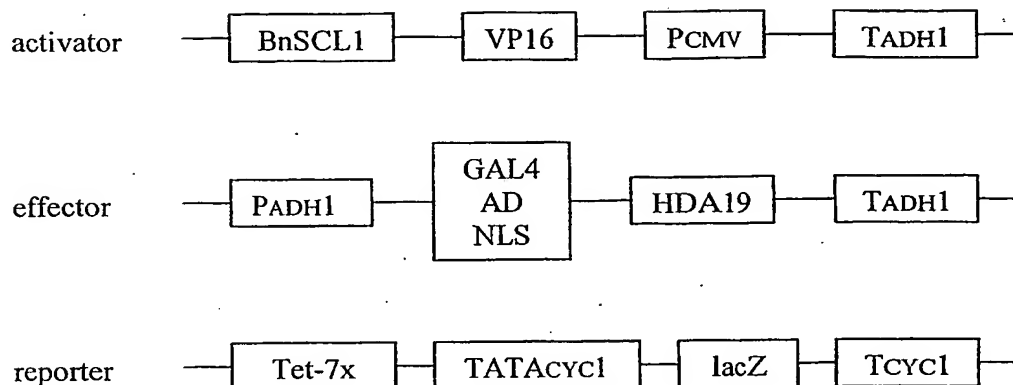


Fig. 29B

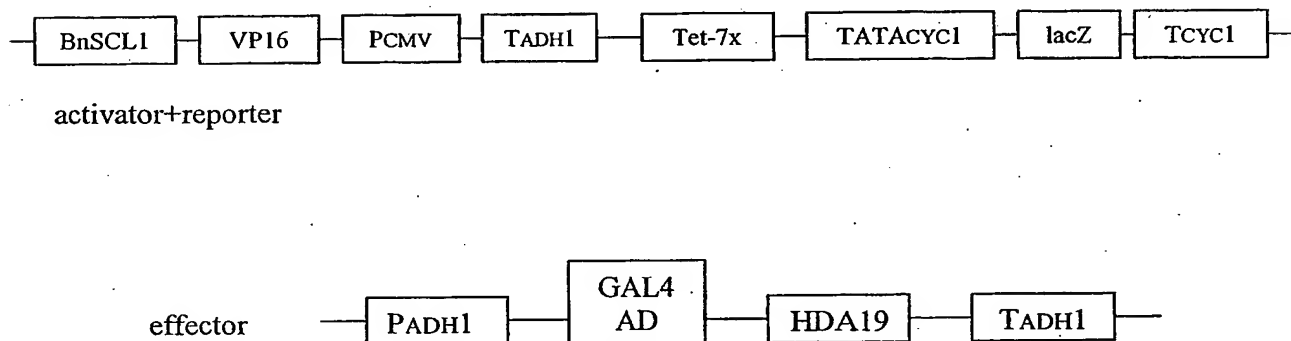


FIG. 29

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